SEQUENCE LISTING

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<120> METHOD

<130> 674509-2025.1

<140> 10/693,234
<141> 2003-10-24

<150> 09/722,938
<151> 2000-11-27

<150> PCT/IB00/01886
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<150> GB 9927801.2
<151> 1999-11-24

<160> 36

<170> PatentIn Ver. 3.2

<210> 1
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
N-terminal amino acid sequence

<400> 1
Ala Thr Leu Pro Gln Lys Asp Pro Gly Tyr
1 5 10

<210> 2
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 2
actccatggc tactttgcca caaaaggacc caggttacat tgttattgac gtcaacgctg 60
g 61

<210> 3
<211> 107
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 3
cgaaatcgat gttggtacca atccatcttc tgttgaaacc ttgcttcatg gatggcaatc 60
ttgggtcagg cttgtctgga gtaccagcgt tgacgtcaat aacaatg 107

<210> 4
<211> 106
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 4
gattggtacc aacatcgatt tcgtttacgt cgtttacact ccacaaggtg cttgtactgc 60
tttggacaga gctatggaaa agtgttctcc aggtaccgtc agaatc 106

<210> 5
<211> 106
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 5
ttcaaccaaa ccagtaacgt tgataatagc cttgacacat tcgtcgaaaa cgaagtcttc 60
gtaacagtga ccaccagaaa cgattctgac ggtacctgga gaacac 106

<210> 6
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 6
atcaacgtta ctggtttggt tgaatctggt tacgacgacg atagaggtta cttcgtctct 60
tccggtgaca ccaactgggg ttccttcaag accttgttca gagaccacgg tagagttttg 120

<210> 7
<211> 109
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 7
caaaccgtgc aatctggcca aaataccgtc acctccaccg acaatgtgac cacccaaacc 60
gacggagtaa caggaaccac ctggcaaaac tctaccgtgg tctctgaac 109

<210> 8
<211> 109
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 8
tttggccaga ttgcacggtt tgccagtcga ttggttatcc ggtgttgaag ttgtcgttaa 60
gccagtcttg accgaagact ctgttcttaa gtacgttcac aaggattcc 109

<210> 9
<211> 116
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 9
ggcaaatcct tgaagtagta tttggtgata ataccgaagt tacctccacc tccaccagtg 60
tgagcccaaa acaactcacc gtcgttacct tcggaatcct tgtgaacgta cttaag 116

<210> 10
<211> 118
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 10
caaatactac ttcaaggatt tgccaatgtc tccaagaggt gtcatcgctt ctaacttaca 60
cttctcttgg gacggtttca ctagagatgc cttgcaagat ttgttgacta agtacttc 118

<210> 11
<211> 118
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 11
ggaggtatac aagtacataa caaactcttc agctgcttgg tggaagattt ggaacttacc 60
aacagtattc ttccaatcac atctagccaa cttgaagtac ttagtcaaca aatcttgc 118

<210> 12
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 12
atcttccatc aggcagctga agagtttgtt atgtacttgt atacatccta ctctaacgac 60
gccgagagag aagttgccca agacagacac tatcat 96

<210> 13
<211> 102
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 13
gaaaggagcc caaccagcat gaccaccaag agctttggta ggctcgcatg ttttgtagat 60
ctgttcaatg tcagcctcca aatgatagtg tctgtcttgg gc 102

<210> 14
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 14
gctggttggg ctcctttccc tgttagacct agacctagac acacatccaa gacttcttat 60
atgcatgacg agactatgga ctacccttc 90

<210> 15
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 15
aatctggaag tctggaaagt ccttgatcat gtaagcagac ttgtacttac ctctctgatt 60
aggaccggaa ccgttgatag tctcagtcaa agcgtagaaa gggtagtcca tagtctcgtc 120

<210> 16
<211> 108
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 16
gactttccag acttccagat tgatgttatc tggaaatacc ttactgaggt tcctgacggt 60
ttgactagtg ccgaaatgaa ggatgctctt cttcaggttg atatgttc 108

<210> 17
<211> 126
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 17
cttgtcttct tcctgccagt atgtctggta ctgcagtttg atgatgtact ctctctgagc 60
aactgcagta gcatcccaaa caaccttgtg aatctcacca ccgaacatat caacctgaag 120
aagagc 126

<210> 18
<211> 108
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 18
acatactggc aggaagaaga caaggatgca gttaacttga agtggattag agacttttac 60
gaggagatgt atgagcctta tggtggtgtt ccagacccta acactcag 108

<210> 19
<211> 111
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 19
ggcaccatac ttaccgttct tccagttgtt caagtcaaca tcagggtagt tgaagtagca 60
tcccctcaaaa acacctttac cactctcaac ctgagtgtta gggtctggaa c 111

<210> 20
<211> 117
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 20
aagaacggta agtatggtgc cttggaactt tacttttttgg gtaacctgaa cagattgatc 60
aaggccaaat ggttgtggga tcctaacgag atcttcacaa acaaacagtc tatccct 117

<210> 21
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 21
gaattccgcg gccgcctact atttagtctg cttaggctcc ttaagaggtt tagtagggat 60
agactgtttg tttgtgaa 78

<210> 22
<211> 1644
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nucleotide
sequence of synthetic Hox gene

<220>
<221> CDS
<222> (1)..(1644)

<400> 22

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atg gct act ttg cca caa aag gac cca ggt tac att gtt att gac gtc   48
Met Ala Thr Leu Pro Gln Lys Asp Pro Gly Tyr Ile Val Ile Asp Val
  1               5                  10                  15

aac gct ggt act cca gac aag cct gac cca aga ttg cca tcc atg aag   96
Asn Ala Gly Thr Pro Asp Lys Pro Asp Pro Arg Leu Pro Ser Met Lys
             20                  25                  30

caa ggt ttc aac aga aga tgg att ggt acc aac atc gat ttc gtt tac  144
Gln Gly Phe Asn Arg Arg Trp Ile Gly Thr Asn Ile Asp Phe Val Tyr
         35                  40                  45

gtc gtt tac act cca caa ggt gct tgt act gct ttg gac aga gct atg  192
Val Val Tyr Thr Pro Gln Gly Ala Cys Thr Ala Leu Asp Arg Ala Met
     50                  55                  60

gaa aag tgt tct cca ggt acc gtc aga atc gtt tct ggt ggt cac tgt  240
Glu Lys Cys Ser Pro Gly Thr Val Arg Ile Val Ser Gly Gly His Cys
 65                  70                  75                  80

tac gaa gac ttc gtt ttc gac gaa tgt gtc aag gct att atc aac gtt  288
Tyr Glu Asp Phe Val Phe Asp Glu Cys Val Lys Ala Ile Ile Asn Val
                 85                  90                  95

act ggt ttg gtt gaa tct ggt tac gac gac gat aga ggt tac ttc gtc  336
Thr Gly Leu Val Glu Ser Gly Tyr Asp Asp Asp Arg Gly Tyr Phe Val
            100                 105                 110

tct tcc ggt gac acc aac tgg ggt tcc ttc aag acc ttg ttc aga gac  384
Ser Ser Gly Asp Thr Asn Trp Gly Ser Phe Lys Thr Leu Phe Arg Asp
        115                 120                 125

cac ggt aga gtt ttg cca ggt ggt tcc tgt tac tcc gtc ggt ttg ggt  432
His Gly Arg Val Leu Pro Gly Gly Ser Cys Tyr Ser Val Gly Leu Gly
    130                 135                 140

ggt cac att gtc ggt gga ggt gac ggt att ttg gcc aga ttg cac ggt  480
Gly His Ile Val Gly Gly Gly Asp Gly Ile Leu Ala Arg Leu His Gly
145                 150                 155                 160

ttg cca gtc gat tgg tta tcc ggt gtt gaa gtt gtc gtt aag cca gtc  528
Leu Pro Val Asp Trp Leu Ser Gly Val Glu Val Val Val Lys Pro Val
                165                 170                 175

ttg acc gaa gac tct gtt ctt aag tac gtt cac aag gat tcc gaa ggt  576
Leu Thr Glu Asp Ser Val Leu Lys Tyr Val His Lys Asp Ser Glu Gly
            180                 185                 190

aac gac ggt gag ttg ttt tgg gct cac act ggt gga ggt gga ggt aac  624
Asn Asp Gly Glu Leu Phe Trp Ala His Thr Gly Gly Gly Gly Gly Asn
        195                 200                 205

ttc ggt att atc acc aaa tac tac ttc aag gat ttg cca atg tct cca  672
Phe Gly Ile Ile Thr Lys Tyr Tyr Phe Lys Asp Leu Pro Met Ser Pro
    210                 215                 220
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aga ggt gtc atc gct tct aac tta cac ttc tct tgg gac ggt ttc act   720
Arg Gly Val Ile Ala Ser Asn Leu His Phe Ser Trp Asp Gly Phe Thr
225                 230                 235                 240

aga gat gcc ttg caa gat ttg ttg act aag tac ttc aag ttg gct aga   768
Arg Asp Ala Leu Gln Asp Leu Leu Thr Lys Tyr Phe Lys Leu Ala Arg
                245                 250                 255

tgt gat tgg aag aat act gtt ggt aag ttc caa atc ttc cac caa gca   816
Cys Asp Trp Lys Asn Thr Val Gly Lys Phe Gln Ile Phe His Gln Ala
            260                 265                 270

gct gaa gag ttt gtt atg tac ttg tat aca tcc tac tct aac gac gcc   864
Ala Glu Glu Phe Val Met Tyr Leu Tyr Thr Ser Tyr Ser Asn Asp Ala
        275                 280                 285

gag aga gaa gtt gcc caa gac aga cac tat cat ttg gag gct gac att   912
Glu Arg Glu Val Ala Gln Asp Arg His Tyr His Leu Glu Ala Asp Ile
    290                 295                 300

gaa cag atc tac aaa aca tgc gag cct acc aaa gct ctt ggt ggt cat   960
Glu Gln Ile Tyr Lys Thr Cys Glu Pro Thr Lys Ala Leu Gly Gly His
305                 310                 315                 320

gct ggt tgg gct cct ttc cct gtt aga cct aga aag aga cac aca tcc   1008
Ala Gly Trp Ala Pro Phe Pro Val Arg Pro Arg Lys Arg His Thr Ser
                325                 330                 335

aag act tct tat atg cat gac gag act atg gac tac cct ttc tac gct   1056
Lys Thr Ser Tyr Met His Asp Glu Thr Met Asp Tyr Pro Phe Tyr Ala
            340                 345                 350

ttg act gag act atc aac ggt tcc ggt cct aat cag aga ggt aag tac   1104
Leu Thr Glu Thr Ile Asn Gly Ser Gly Pro Asn Gln Arg Gly Lys Tyr
        355                 360                 365

aag tct gct tac atg atc aag gac ttt cca gac ttc cag att gat gtt   1152
Lys Ser Ala Tyr Met Ile Lys Asp Phe Pro Asp Phe Gln Ile Asp Val
    370                 375                 380

atc tgg aaa tac ctt act gag gtt cct gac ggt ttg act agt gcc gaa   1200
Ile Trp Lys Tyr Leu Thr Glu Val Pro Asp Gly Leu Thr Ser Ala Glu
385                 390                 395                 400

atg aag gat gct ctt ctt cag gtt gat atg ttc ggt ggt gag att cac   1248
Met Lys Asp Ala Leu Leu Gln Val Asp Met Phe Gly Gly Glu Ile His
                405                 410                 415

aag gtt gtt tgg gat gct act gca gtt gct cag aga gag tac atc atc   1296
Lys Val Val Trp Asp Ala Thr Ala Val Ala Gln Arg Glu Tyr Ile Ile
            420                 425                 430

aaa ctg cag tac cag aca tac tgg cag gaa gaa gac aag gat gca gtt   1344
Lys Leu Gln Tyr Gln Thr Tyr Trp Gln Glu Glu Asp Lys Asp Ala Val
        435                 440                 445
```

```
aac ttg aag tgg att aga gac ttt tac gag gag atg tat gag cct tat   1392
Asn Leu Lys Trp Ile Arg Asp Phe Tyr Glu Glu Met Tyr Glu Pro Tyr
    450                 455                 460

ggt ggt gtt cca gac cct aac act cag gtt gag agt ggt aaa ggt gtt   1440
Gly Gly Val Pro Asp Pro Asn Thr Gln Val Glu Ser Gly Lys Gly Val
465                 470                 475                 480

ttt gag gga tgc tac ttc aac tac cct gat gtt gac ttg aac aac tgg   1488
Phe Glu Gly Cys Tyr Phe Asn Tyr Pro Asp Val Asp Leu Asn Asn Trp
                485                 490                 495

aag aac ggt aag tat ggt gcc ttg gaa ctt tac ttt ttg ggt aac ctg   1536
Lys Asn Gly Lys Tyr Gly Ala Leu Glu Leu Tyr Phe Leu Gly Asn Leu
            500                 505                 510

aac aga ttg atc aag gcc aaa tgg ttg tgg gat cct aac gag atc ttc   1584
Asn Arg Leu Ile Lys Ala Lys Trp Leu Trp Asp Pro Asn Glu Ile Phe
        515                 520                 525

aca aac aaa cag tct atc cct act aaa cct ctt aag gag cct aag cag   1632
Thr Asn Lys Gln Ser Ile Pro Thr Lys Pro Leu Lys Glu Pro Lys Gln
    530                 535                 540

act aaa tag tag                                                  1644
Thr Lys
545
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<210> 23
<211> 546
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amino acid sequence of synthetic Hox gene

<400> 23

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Met Ala Thr Leu Pro Gln Lys Asp Pro Gly Tyr Ile Val Ile Asp Val
  1               5                  10                  15

Asn Ala Gly Thr Pro Asp Lys Pro Asp Pro Arg Leu Pro Ser Met Lys
            20                  25                  30

Gln Gly Phe Asn Arg Arg Trp Ile Gly Thr Asn Ile Asp Phe Val Tyr
        35                  40                  45

Val Val Tyr Thr Pro Gln Gly Ala Cys Thr Ala Leu Asp Arg Ala Met
    50                  55                  60

Glu Lys Cys Ser Pro Gly Thr Val Arg Ile Val Ser Gly Gly His Cys
65                  70                  75                  80

Tyr Glu Asp Phe Val Phe Asp Glu Cys Val Lys Ala Ile Ile Asn Val
                85                  90                  95
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```
Thr Gly Leu Val Glu Ser Gly Tyr Asp Asp Asp Arg Gly Tyr Phe Val
            100                 105                 110

Ser Ser Gly Asp Thr Asn Trp Gly Ser Phe Lys Thr Leu Phe Arg Asp
        115                 120                 125

His Gly Arg Val Leu Pro Gly Gly Ser Cys Tyr Ser Val Gly Leu Gly
    130                 135                 140

Gly His Ile Val Gly Gly Gly Asp Gly Ile Leu Ala Arg Leu His Gly
145                 150                 155                 160

Leu Pro Val Asp Trp Leu Ser Gly Val Glu Val Val Val Lys Pro Val
                165                 170                 175

Leu Thr Glu Asp Ser Val Leu Lys Tyr Val His Lys Asp Ser Glu Gly
            180                 185                 190

Asn Asp Gly Glu Leu Phe Trp Ala His Thr Gly Gly Gly Gly Gly Asn
        195                 200                 205

Phe Gly Ile Ile Thr Lys Tyr Tyr Phe Lys Asp Leu Pro Met Ser Pro
    210                 215                 220

Arg Gly Val Ile Ala Ser Asn Leu His Phe Ser Trp Asp Gly Phe Thr
225                 230                 235                 240

Arg Asp Ala Leu Gln Asp Leu Leu Thr Lys Tyr Phe Lys Leu Ala Arg
                245                 250                 255

Cys Asp Trp Lys Asn Thr Val Gly Lys Phe Gln Ile Phe His Gln Ala
            260                 265                 270

Ala Glu Glu Phe Val Met Tyr Leu Tyr Thr Ser Tyr Ser Asn Asp Ala
        275                 280                 285

Glu Arg Glu Val Ala Gln Asp Arg His Tyr His Leu Glu Ala Asp Ile
    290                 295                 300

Glu Gln Ile Tyr Lys Thr Cys Glu Pro Thr Lys Ala Leu Gly Gly His
305                 310                 315                 320

Ala Gly Trp Ala Pro Phe Pro Val Arg Pro Arg Lys Arg His Thr Ser
                325                 330                 335

Lys Thr Ser Tyr Met His Asp Glu Thr Met Asp Tyr Pro Phe Tyr Ala
            340                 345                 350

Leu Thr Glu Thr Ile Asn Gly Ser Gly Pro Asn Gln Arg Gly Lys Tyr
        355                 360                 365

Lys Ser Ala Tyr Met Ile Lys Asp Phe Pro Asp Phe Gln Ile Asp Val
    370                 375                 380

Ile Trp Lys Tyr Leu Thr Glu Val Pro Asp Gly Leu Thr Ser Ala Glu
385                 390                 395                 400
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```
Met Lys Asp Ala Leu Leu Gln Val Asp Met Phe Gly Gly Glu Ile His
                405                 410                 415

Lys Val Val Trp Asp Ala Thr Ala Val Ala Gln Arg Glu Tyr Ile Ile
            420                 425                 430

Lys Leu Gln Tyr Gln Thr Tyr Trp Gln Glu Glu Asp Lys Asp Ala Val
        435                 440                 445

Asn Leu Lys Trp Ile Arg Asp Phe Tyr Glu Glu Met Tyr Glu Pro Tyr
    450                 455                 460

Gly Gly Val Pro Asp Pro Asn Thr Gln Val Glu Ser Gly Lys Gly Val
465                 470                 475                 480

Phe Glu Gly Cys Tyr Phe Asn Tyr Pro Asp Val Asp Leu Asn Asn Trp
                485                 490                 495

Lys Asn Gly Lys Tyr Gly Ala Leu Glu Leu Tyr Phe Leu Gly Asn Leu
            500                 505                 510

Asn Arg Leu Ile Lys Ala Lys Trp Leu Trp Asp Pro Asn Glu Ile Phe
        515                 520                 525

Thr Asn Lys Gln Ser Ile Pro Thr Lys Pro Leu Lys Glu Pro Lys Gln
    530                 535                 540

Thr Lys
545
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<210> 24
<211> 5
<212> PRT
<213> Schwanniomyces occidentalis

<400> 24
Ser Ala Ile Gln Ala
  1   5

<210> 25
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      amino acid signal sequence

<400> 25
Met Ala Thr Leu Pro
  1   5

<210> 26
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic amino acid signal sequence

<400> 26
Ala Thr Leu Pro
1

<210> 27
<211> 6
<212> PRT
<213> Saccharomyces cerevisiae

<400> 27
Lys Arg Glu Ala Glu Ala
1 5

<210> 28
<211> 5
<212> PRT
<213> Aspergillus oryzae

<400> 28
Ala Pro Ala Leu Ala
1 5

<210> 29
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 29
gaattcatga ccgcattgtc cgacaaacaa acggct 36

<210> 30
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 30
acccggggta gaagagccgg cagcaaacca gtt 33

<210> 31
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 31
gggtgagctc tgccacttcc agggctgcgc tgttc 35

<210> 32
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 32
ggagatcttt attaatggtg atggtgatgg tgggtaattg tgatcacagc gtccgg 56

<210> 33
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 33
ggagatacta cctggaactc tggacaagag gac 33

<210> 34
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 34
gtttggatcc ccgccagtac ccac 24

<210> 35
<211> 20
<212> PRT
<213> Hansenula polymorpha

<400> 35
Gly Ser Thr Asp Asn Pro Asp Gly Ile Asp Tyr Lys Thr Tyr Asp Tyr
1 5 10 15

Val Gly Val Trp
20

<210> 36
<211> 31
<212> PRT
<213> Gracilariopsis lemaneiformis

<400> 36
Thr Ala Leu Ser Asp Lys Gln Thr Ala Thr Ala Gly Ser Thr Asp Asn
1 5 10 15

Pro Asp Gly Ile Asp Tyr Lys Thr Tyr Asp Tyr Val Gly Val Trp
20 25 30